

NEW SHEET

(3) Sequence Description: Figure 11A

1	ATGTCCCCTATACTAGGTTATTGGAAAATTAAGGGCCTTGTGCAACCC	
5	MetSerProIleLeuGlyTyrTrpLysIleLysGlyLeuValGlnPro	16
49	ACTCGACTTCTTTTGGGAATATCTTGAAGAAAAATATGAAGAGCATTTG	
	ThrArgLeuLeuLeuGluTyrLeuGluGluLysTyrGluGluHisLeu	32
10	97 TATGAGCGCGATGAAGGTGATAAATGGCGAAACAAAAGTTTGAATTG	
	TyrGluArgAspGluGlyAspLysTrpArgAsnLysLysPheGluLeu	48
145	GGTTTGGAGTTTCCCAATCTTCCTTATTATATTGATGGTGATGTTAAA	
	GlyLeuGluPheProAsnLeuProTyrTyrIleAspGlyAspValLys	64
15	193 TTAACACAGTCTATGGCCATCATACGTTATATAGCTGACAAGCACAAAC	
	LeuThrGlnSerMetAlaIleIleArgTyrIleAlaAspLysHisAsn	80
241	ATGTTGGGTGGTTGTCCAAAAGAGCGTGCAGAGATTTCAATGCTTGAA	
20	MetLeuGlyGlyCysProLysGluArgAlaGluIleSerMetLeuGlu	96
289	GGAGCGGTTTTGGATATTAGATACGGTGTTCGAGAATTGCATATAGT	
	GlyAlaValLeuAspIleArgTyrGlyValSerArgIleAlaTyrSer	112
337	AAAGACTTTGAAACTCTCAAAGTTGATTTTCTTAGCAAGCTACCTGAA	
25	LysAspPheGluThrLeuLysValAspPheLeuSerLysLeuProGlu	128
385	ATGCTGAAAATGTTCTGAAGATCGTTTATGTCATAAAACATATTTAAAT	
	MetLeuLysMetPheGluAspArgLeuCysHisLysThrTyrLeuAsn	144
433	GGTGATCATGTAACCCATCCTGACTTCATGTTGTATGACGCTCTTGAT	
	GlyAspHisValThrHisProAspPheMetLeuTyrAspAlaLeuAsp	160
481	GTTGTTTTATACATGGACCCAATGTGCCTGGATGCGTTCCCAAAATTA	
35	ValValLeuTyrMetAspProMetCysLeuAspAlaPheProLysLeu	176

NEW SHEET

(3) Sequence Description (continued): Figure 11B

529 GTTTGTTTTAAAAACGTATTGAAGCTATCCCACAAATTGATAAGTAC
ValCysPheLysLysArgIleGluAlaIleProGlnIleAspLysTyr 192

5 577 TTGAAATCCAGCAAGTATATAGCATGGCCTTTGCAGGGCTGGCAAGCC
LeuLysSerSerLysTyrIleAlaTrpProLeuGlnGlyTrpGlnAla 208

625 ACGTTTGGTGGTGGCGACCATCCTCCAAAATCGGATCTGGTTCGCGT
ThrPheGlyGlyGlyAspHisProProLysSerAspLeuValProArg 224

10 673 GGATCCATGAGCACGATTCCCAAACCTCAAAGAAAAACCAAACGTAAC
GlySerMetSerThrIleProLysProGlnArgLysThrLysArgAsn 240

15 721 ACCAACCGTCGCCCCACAGGAATTCATCGTGACTGACTGA
ThrAsnArgArgProGlnGluPheIleValThrAspEnd 252

NEW SHEET

(4) Sequence Description: Figure 12A

1	ATGTCCCCTATACTAGGTTATTGGAAAATTAAGGGCCTTGTGCAACCC	
	MetSerProIleLeuGlyTyrTrpLysIleLysGlyLeuValGlnPro	16
5	49 ACTCGACTTCTTTTGAATATCTTGAAGAAAAATATGAAGAGCATTTG	
	ThrArgLeuLeuLeuGluTyrLeuGluGluLysTyrGluGluHisLeu	32
	97 TATGAGCGCGATGAAGGTGATAAATGGCGAAACAAAAAGTTTGAATTG	
	TyrGluArgAspGluGlyAspLysTrpArgAsnLysLysPheGluLeu	48
10	145 GGT TTGGAGTTTCCCAATCTTCCTTATTATATTGATGGTGATGTTAAA	
	GlyLeuGluPheProAsnLeuProTyrTyrIleAspGlyAspValLys	64
	193 TTAACACAGTCTATGGCCATCATACGTTATATAGCTGACAAGCACAAAC	
	LeuThrGlnSerMetAlaIleIleArgTyrIleAlaAspLysHisAsn	80
15	241 ATGTTGGGTGGTTGTCCAAAAGAGCGTGCAGAGATTTCAATGCTTGAA	
	MetLeuGlyGlyCysProLysGluArgAlaGluIleSerMetLeuGlu	96
20	289 GGAGCGGTTTTGGATATTAGATACGGTGTTTCGAGAATTGCATATAGT	
	GlyAlaValLeuAspIleArgTyrGlyValSerArgIleAlaTyrSer	112

NEW SHEET

(4) Sequence Description (continued): Figure 12B

337	AAAGACTTTGAAACTCTCAAAGTTGATTTTCTTAGCAAGCTACCTGAA	
	LysAspPheGluThrLeuLysValAspPheLeuSerLysLeuProGlu	128
5	385 ATGCTGAAAATGTTCTGAAGATCGTTTATGTCATAAAACATATTTAAAT	
	MetLeuLysMetPheGluAspArgLeuCysHisLysThrTyrLeuAsn	144
	433 GGTGATCATGTAACCCATCCTGACTTCATGTTGTATGACGCTCTTGAT	
	GlyAspHisValThrHisProAspPheMetLeuTyrAspAlaLeuAsp	160
10		
	481 GTTGTTTTTATACATGGACCCAATGTGCCTGGATGCGTTCCCAAATTA	
	ValValLeuTyrMetAspProMetCysLeuAspAlaPheProLysLeu	176
	529 GTTTGTTTTAAAAACGTATTGAAGCTATCCCACAAATTGATAAGTAC	
15	ValCysPheLysLysArgIleGluAlaIleProGlnIleAspLysTyr	192
	577 TTGAAATCCAGCAAGTATATAGCATGGCCTTTGCAGGGCTGGCAAGCC	
	LeuLysSerSerLysTyrIleAlaTrpProLeuGlnGlyTrpGlnAla	208
20	625 ACGTTTGGTGGTGGCGACCATCCTCCAAAATCGGATCTGGTTCCGCGT	
	ThrPheGlyGlyGlyAspHisProProLysSerAspLeuValProArg	224
	673 GGATCCGACGTCAAGTTCCCGGGTGGCGGTCAGATCGTTGGTGGAGTT	
	GlySerAspValLysPheProGlyGlyGlyGlnIleValGlyGlyVal	240
25		
	721 TACTTGTTGCCGCGCAGGGAATTCATCGTGACTGACTGA	
	TyrLeuLeuProArgArgGluPheIleValThrAspEnd	252

NEW SHEET

5

(6) Sequence Description: Figure 13A

1	ATGTCCCCTATACTAGGTTATTGGAAAATTAAGGGCCTTGTGCAACCC	
	MetSerProIleLeuGlyTyrTrpLysIleLysGlyLeuValGlnPro	16
10	49 ACTCGACTTCTTTTGGAAATATCTTGAAGAAAAATATGAAGAGCATTTG	
	ThrArgLeuLeuLeuGluTyrLeuGluGluLysTyrGluGluHisLeu	32
	97 TATGAGCGCGATGAAGGTGATAAATGGCGAAACAAAAAGTTTGAATTG	
	TyrGluArgAspGluGlyAspLysTrpArgAsnLysLysPheGluLeu	48
15	145 GGT TTGGAGTTTCCCAATCTTCCTTATTATATTGATGGTGATGTTAAA	
	GlyLeuGluPheProAsnLeuProTyrTyrIleAspGlyAspValLys	64
	193 TTAACACAGTCTATGGCCATCATACGTTATATAGCTGACAAGCACAAC	
20	LeuThrGlnSerMetAlaIleIleArgTyrIleAlaAspLysHisAsn	80
	241 ATGTTGGGTGGTTGTCCAAAAGAGCGTGCAGAGATTTCAATGCTTGAA	
	MetLeuGlyGlyCysProLysGluArgAlaGluIleSerMetLeuGlu	96
25	289 GGAGCGGTTTTGGATATTAGATACGGTGTTCGAGAATTGCATATAGT	
	GlyAlaValLeuAspIleArgTyrGlyValSerArgIleAlaTyrSer	112
	337 AAAGACTTTGAAACTCTCAAAGTTGATTTTCTTAGCAAGCTACCTGAA	
	LysAspPheGluThrLeuLysValAspPheLeuSerLysLeuProGlu	128
30	385 ATGCTGAAAATGTTTGAAGATCGTTTATGTCATAAAACATATTTAAAT	
	MetLeuLysMetPheGluAspArgLeuCysHisLysThrTyrLeuAsn	144
	433 GGTGATCATGTAACCCATCCTGACTTCATGTTGTATGACGCTCTTGAT	
35	GlyAspHisValThrHisProAspPheMetLeuTyrAspAlaLeuAsp	160

NEW SHEET

(6) Sequence Description (continued): Figure 13B

481	GTTGTTTTTATACATGGACCCAATGTGCCTGGATGCGTTCCCAAAATTA	
	ValValLeuTyrMetAspProMetCysLeuAspAlaPheProLysLeu	176
5	529 GTTTGTTTTTAAAAACGTATTGAAGCTATCCCACAAATTGATAAGTAC	
	ValCysPheLysLysArgIleGluAlaIleProGlnIleAspLysTyr	192
	577 TTGAAATCCAGCAAGTATATAGCATGGCCTTTGCAGGGCTGGCAAGCC	
	LeuLysSerSerLysTyrIleAlaTrpProLeuGlnGlyTrpGlnAla	208
10	625 ACGTTTGGTGGTGGCGACCATCCTCCAAAATCGGATCTGGTTCCGCGT	
	ThrPheGlyGlyGlyAspHisProProLysSerAspLeuValProArg	224
	673 GGATCCAGCACGATTCCCAAACCTCAAAGAAAAACCAAACGTAACACC	
	GlySerSerThrIleProLysProGlnArgLysThrLysArgAsnThr	240
15	721 AACCGTCGCCCACAGGACGTCAAGTTCCCGGGTGGCGGTCAGATCGTT	
	AsnArgArgProGlnAspValLysPheProGlyGlyGlyGlnIleVal	256
	769 GGTGGAGTTTACTTGTTGCCGCGCAGGGAATTCATCGTGACTGACTGA	
20	GlyGlyValTyrLeuLeuProArgArgGluPheIleValThrAspEnd	271

NEW SHEET

(7) Sequence Description: Figure 14

5'-GATCCATGAGCACGATTCCCAAACCTCAAAGAAAAACCAAACGTAACACCAACCGTCGC
CCACAGG-3'

5 (8) Sequence Description: Figure 15

5'-AATTCCTGTGGGCGACGGTTGGTGTTACGTTTGGTTTTCTTTGAGGTTTGGGAATCGT
GCTCATG-3'

(9) Sequence Description: Figure 16

10 5'-GATCCGACGTCAAGTTCCCGGGTGGCGGTCAGATCGTTGGTGGAGTTTACTTGTTGCCG
CGCAGGG-3'

(10) Sequence Description: Figure 17

15 5'-AATTCCTGCGCGGCAACAAGTAAACTCCACCAACGATCTGACCGCCACCCGGGAATT
GACGTCG-3'

(13) Sequence Description: Figure 18

5'-GAATTCTTACCTGCGCGGCAACAAGTAAACTC-3'

20 (14) Sequence Description: Figure 19

5'-GCTGGATCCAGCACGATTCCCAAACCTCAAAG-3'